High-throughput epitope identification for snakebite antivenom

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High-throughput epitope identification for snakebite antivenom

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Introduction

Insight into the epitopic recognition pattern for polyclonal antivenoms is a strong tool for accurate prediction of antivenom cross-reactivity and provides a basis for design of novel antivenoms. In this work, a high-throughput approach was applied to characterize linear epitopes in 966 individual toxins from pit vipers (Crotalidae) using the ICP Crotalidae antivenom. Due to an abundance of snake venom metalloproteinases and phospholipase A₂ in the venoms used for production of the investigated antivenom, this study focuses on these toxin families.

Objectives

- Identify epitopes in toxins used in immunization
- Characterize tolerated amino acid substitutions in identified epitopes
- Predict cross-reactivity of antivenom

Immunization mixture

To identify the epitopes observed for specific signal intensities were mapped back to the amino acid sequence of each pit viper toxin. Using two or more overlapping 15-mer peptides with median signals above 20 AU, epitope core sequences were localized to the amino acid sequence of each pit viper toxin. Using two or more overlapping 15-mer peptides with median signals above 20 AU, epitope core sequences were localized to the amino acid sequence of each pit viper toxin. Using two or more overlapping 15-mer peptides with median signals above 20 AU, epitope core sequences were localized to the amino acid sequence of each pit viper toxin.

Epitopes locate to surface regions

The epitope core sequences are highlighted in blue except for the high-signal epitope in Bothrops asper P-I metalloproteinase that is highlighted in red. All epitopes are found to be exposed on the protein surface. The structure of the metalloproteinase (PDB: 2W11) was obtained from the Protein Data Bank (pdb.org), and the homology model of the phospholipase A₂ was built using CPHmodels® based on a crystal structure of the lysphospholipase from B. jararaca (PDB: 4KF3) with 87.7% identity.

Conclusions

- Custom-designed high density peptide microarray technology enables parallel automated identification of epitopes in hundreds of toxins.
- Integrating multiple sequence alignment allows investigation of the effect of epitope variation on antivenom recognition.
- Cross-reactIVITY of antivenom is correlated to the degree of conservation in toxin epitopes and flanking residues.

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